67. ~~58~~. (New) A host cell transformed by the vector of claim 52.

68. ~~54~~. (New) The host cell of claim 53, wherein the host cell is a prokaryotic cell.

69. ~~55~~. (New) The host cell of claim 53, wherein the host cell is a eukaryotic cell.

70. ~~56~~. (New) A method for producing the nucleic acid sequence of claim 48, the method comprising growing a host cell, the host cell comprising a vector comprising the nucleic acid sequence of claim 48, and isolating the nucleic acid sequence from said culture.

71. ~~57~~. (New) The method of claim 56, wherein the host cell is a prokaryotic cell.

72. ~~58~~. (New) The method of claim 56, wherein the host cell is a eukaryotic cell.

Remarks

Claims 1-16, 19-21 and 25-29 were pending in this case. With the above amendments, applicants cancel all pending claims 1-16, 19-21 and 25-29 without prejudice or disclaimer and substitute therefor new claims 30-58. The amendments are made to more particularly point out and distinctly claim the invention.

The claim amendments provide no new matter. The claim elements that may not be present in previously filed claims find support in the specification as follows:

Support for the 1362 nucleotides of claim 30 is found at least at page 8, line 18.

Support for "high stringency conditions" of claims 30-33 is found at least at page 8, lines 27-29.

Support for "complements" of sequences is found at least at page 9, in several places in the top partial paragraph.

Support for the twelve transmembrane domains and hydropathy plot of claim 34 is found at least at page 40, lines 1-3.

Support for the "11 to 1372 nucleotides of SEQ ID NO:6" of claim 39 is found at least at page 8, lines 17-18, as informed by Figure 9 and the sequence listing.

Support for "expression of the sequence is increased in a mammal in response to hyperglycemia or insulinopenia" of claim 45 is found at least at page 39, lines 26-28.

Rejections under 35 U.S.C. 101 and 35 U.S.C. 112, first paragraph

All claims stand rejected under 35 U.S.C. 101 and 35 U.S.C. 112, first paragraph as lacking utility and enablement. It is asserted that the specification fails to establish that the disclosed polynucleotide sequences encode a protein which is a member of the glucose transporter/sensor/receptor family. Applicants respectfully request reconsideration and withdrawal of these rejections in light of the claim amendments and the following discussion.

The PTO asserts that the sequences are simply computer generated hypotheses, wherein no biological function has been established. However, applicants contend that the specification provides sufficient evidence to establish to the skilled artisan that the disclosed nucleotide sequences (SEQ ID Nos 6, 9 and 11) are portions of sequences encoding human, mouse and rat versions, respectively, of a novel member of the GLUT family (designated GLUTx).

The PTO first asserts that the apparent partial sequences have not been shown to have GLUTx activity. Applicants first note that the claims as amended do not require that the sequences provided have GLUTx activity. Additionally, the partial sequences

provided would be understood to be the majority portions of an active GLUTx, based on the following evidence:

- The sequences provided have significant homology to other GLUT family members. Although the PTO characterizes this homology as low, applicants note that the homology values (23% to 40%) are values that would be expected between various members of the GLUT family. See, e.g., Ibberson et al., 2000, J. Biol. Chem. 275:4607-4612, provided with the March 1, 2002 Office Action, where the abstract notes that the GLUTX1 glucose transporter has between 29 and 32% identity with rat GLUT1-5 and 32-36% identity with plant and bacterial hexose transporters. Additionally, Doege et al., 2000, J. Biol Chem. 275:16275-16280, also provided with the March 1, 2002 Office Action, indicates in the abstract that the GLUT8 transporter is 29.4% identical with GLUT1. Moreover, the GLUTx sequences were found using degenerate primers corresponding to conserved areas of known glucose transporters. Therefore, the GLUTx sequences share homology to known glucose transporters at regions where homology would be expected. In light of the specification, Ibberson et al. and Doege et al., the skilled artisan would understand that the identities provided in the instant specification for GLUTx would be expected for a novel glucose transporter. Those identity values thus would provide evidence to a skilled artisan that the disclosed sequences are indeed for a novel glucose transporter.
- The disclosed GLUTx sequences are expressed where expected for glucose transporters. See page 34, lines 12-19; page 38, lines 23-25; page 39, lines 4-8. Additionally, GLUTx mRNA is upregulated in response to streptozotocin and under hyperglycemia and insulinopenia - page 39, lines 15-30.

- Hydropathy plot analysis of the primary sequence of GLUTx establishes that the protein has 12 transmembrane domains, as expected for a glucose transporter.

Thus, since several lines of evidence, including structural, homology, and expression data are consistent with the assertion that the provided sequences are indeed sequences of a novel glucose transporter, the specification provides much more evidence than merely a "computer generated hypothesis". The hypothesis was actually tested, and all evidence provided is consistent with the assertion that the disclosed sequences are that of a novel glucose transporter. Indeed, the skilled artisan would understand that the data in the specification provides a strong case for that assertion.

As such, the claims have sufficient utility to overcome the present rejection, since the claimed nucleic acids can be used, e.g., for probes (as claimed and as disclosed on page 15, lines 6-26) to detect abnormal expression of GLUTx, as well as for evaluating the effect of GLUTx under various conditions. The skilled artisan would also recognize from the specification as filed that the claimed compositions have specific and credible utility.

With regard to the aspect of these rejections discussed on page 6-8 of the March 1, 2002 Office Action, Applicants note that the claims as amended do not encompass variants of GLUTx, but only claim what is described in the application, including sequences that bind under high stringency to the exemplified sequences.

In light of the above discussion, applicants respectfully request withdrawal of the utility/written description rejections under 35 U.S.C. 101 and 112, first paragraph.

Rejections under 35 U.S.C. 112, second paragraph

Claims 1-16, 19-21 and 25-29 stand rejected under 35 U.S.C. 112, second paragraph as being indefinite because it is asserted to be unclear what the metes and

bounds of GLUTx is. Applicants respectfully request withdrawal of these rejections because the rejected claims have been cancelled and the new claims no longer specify "GLUTx".

Rejections under 35 U.S.C. 102

Claims 1-2, 4-5, 12-13, and 20-21 stand rejected under 35 U.S.C. 102(b) as being anticipated by Lee et al., disclosing EST H34451 and H34372. Additionally, claim 19 is rejected as being anticipated by the following GenBank accession numbers, as recited by Adams et al.: G20347, AB005878, and CCRHOD. Applicants respectfully request reconsideration and withdrawal of these rejections based on the following discussion.

Applicants first note that the rejected claims have been cancelled. Applicants also assert that the new claims 30-58 are not anticipated by the cited EST or GenBank sequences because claim 30 does not encompass those EST or GenBank sequences and all other claims are dependent on claim 30. Specifically, claim 30 requires that the claimed nucleic acid sequence comprise at least 1362 nucleotides. The cited EST sequences do not comprise at least 1362 nucleotides, and therefore cannot anticipate the claimed sequences.

Rejections under 35 U.S.C. 103(a)

Claims 14-16 stand rejected under 35 U.S.C. 103(a) as being unpatentable over Lee et al., disclosing EST sequences H34451 and H34372, in view of Ausubel. As with the rejections under 35 U.S.C. 102(b) discussed above, applicants respectfully request reconsideration and withdrawal of these rejections because the rejected claims are no longer pending. Additionally, the current claims are not obvious in light of the above EST sequences in view of Ausubel because the combination of those sequences and

Ausubel do not make obvious a sequence of at least 1362 nucleotides, as required by the claims, because those EST sequences are substantially shorter than 1362 nucleotides and there is no suggestion that they are part of a sequence of 1362 nucleotides that have specific utility.

Conclusion

In light of the claim amendments and the above remarks, applicants respectfully request withdrawal of all objections and rejections and passage of the currently pending claims 30-58 to allowance. If there are any minor matters that would prevent allowance of the claims, applicants request that the Examiner contact the undersigned attorney.

It is believed no fee is required to maintain the pendency of this application. However, if there are unanticipated fees required to maintain the pendency of this application, the PTO is authorized to withdraw those fees from Deposit Account 01-1785. Overcharges may also be credited to Deposit Account 01-1785.

Respectfully submitted,

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Dated: New York, New York
June 3, 2002

By: _____
Elie H. Gendloff
Registration No.: 44,704

Currently Pending Claims - 09/516,493
All claims are new.

30. (New) An isolated nucleic acid sequence, the sequence comprising at least 1362 nucleotides, that hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:11, the complement of SEQ ID NO:6, the complement of SEQ ID NO:9, and the complement of SEQ ID NO:11.

31. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence hybridizes under high stringency conditions to SEQ ID NO:6 or the complement of SEQ ID NO:6.

32. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence hybridizes under high stringency conditions to SEQ ID NO:9 or the complement of SEQ ID NO:9.

33. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence hybridizes under high stringency conditions to SEQ ID NO:11 or the complement of SEQ ID NO:11.

34. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence or its complement encodes an amino acid sequence comprising 12 transmembrane domains, as determined by hydropathy plot analysis.

35. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence is identical or complementary to at least a portion of SEQ ID NO:6.

36. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence is identical or complementary to at least a portion of SEQ ID NO:9.

37. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence is identical or complementary to at least a portion of SEQ ID NO:11.

38. (New) The isolated nucleic acid sequence of claim 30, wherein the sequence is identical or complementary to SEQ ID NO:6.

39. (New) The isolated nucleic acid sequence of claim 35, wherein the sequence comprises nucleotides 11 to 1372 of SEQ ID NO:6.

40. (New) The isolated nucleic acid sequence of claim 38, comprising SEQ ID NO:6.

41. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence encodes SEQ ID NO:7.

42. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence encodes SEQ ID NO:10.

43. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence encodes SEQ ID NO:12.

44. (New) The isolated nucleic acid sequence of claim 41, wherein the amino acid sequence is SEQ ID NO:7.

45. (New) The isolated nucleic acid sequence of claim 30, wherein expression of the sequence is increased in a mammal in response to hyperglycemia or insulinopenia.

46. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence is RNA.

47. (New) The isolated nucleic acid sequence of claim 46, wherein the RNA is mRNA.

48. (New) The isolated nucleic acid sequence of claim 30, wherein the nucleic acid sequence is DNA.

49. (New) The isolated nucleic acid sequence of claim 48, wherein the nucleic acid sequence is cDNA.

50. (New) A probe comprising the nucleic acid sequence of claim 30, wherein the nucleic acid sequence is labeled.

51. (New) The probe of claim 50, wherein the nucleic acid sequence is labeled with a radioactive label.

52. (New) A vector comprising the nucleic acid sequence of claim 48.

53. (New) A host cell transformed by the vector of claim 52.

54. (New) The host cell of claim 53, wherein the host cell is a prokaryotic cell.

55. (New) The host cell of claim 53, wherein the host cell is a eukaryotic cell.

56. (New) A method for producing the nucleic acid sequence of claim 48, the method comprising growing a host cell, the host cell comprising a vector comprising the nucleic acid sequence of claim 48, and isolating the nucleic acid sequence from said culture.

57. (New) The method of claim 56, wherein the host cell is a prokaryotic cell.

58. (New) The method of claim 56, wherein the host cell is a eukaryotic cell.

06-04-02

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I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Commissioner for Patents, Washington, D.C. 20231.
Name: Elie H. Gendloff
Signature: [signature]

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Commissioner for Patents
Washington, DC 20231

Box NON-FEE AMENDMENT

Re: U.S. Utility Patent Application Serial No. 09/516,493
Title: NOVEL GLUCOSE TRANSPORTER/SENSOR PROTEIN AND USES THEREOF
Inventors: Maureen J. Charron and Ellen B. Katz
Our File: 96700/613

Dear Sir:

Enclosed please find the following documents for filing with the above-identified utility patent application in the names of Maureen J. Charron and Ellen B. Katz, entitled NOVEL GLUCOSE TRANSPORTER/SENSOR PROTEIN AND USES THEREOF, comprising the following:

1. a Reply and Amendment under 37 C.F.R. 1.111 in response to the March 1, 2002 Office Action (10 pages) and attached thereto Currently Pending Claims (4 pages); and

2. a Return receipt postcard.

Small entity status was previously established and is still proper.

Please acknowledge receipt of the enclosed papers by stamping the enclosed postcard and returning the same to us.

Respectfully submitted,

AMSTER, ROTHSTEIN & EBENSTEIN
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Dated: June 3, 2002
New York, New York

By: [signature]
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